

Patent

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and Its Uses

<130> 5718-34, 035718-174234

<140>

<141>

<150> 60/072,785

<151> 1998-01-27

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2949

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2949)

<400> 1

atg gcg gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg 48
Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Ieu
20 25 30

cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

atg tgg aac cat gcc agg tgc atc ttc agc aag aac cag ata aaa 192
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct			288
Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser			
85	90	95	
aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc			336
Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala			
100	105	110	
cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc			384
Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val			
115	120	125	
cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg			432
Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp			
130	135	140	
tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag			480
Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu			
145	150	155	160
aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg			528
Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met			
165	170	175	
ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt			576
Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly			
180	185	190	
tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc			624
Ser Lys Arg Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala			
195	200	205	
agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa			672
Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln			
210	215	220	
ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta			720
Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu			
225	230	235	240
aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt			768
Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu			
245	250	255	
aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat			816
Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn			
260	265	270	

ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg			864
Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala			
275	280	285	
gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat			912
Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn			
290	295	300	
ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca			960
Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser			
305	310	315	320
gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag			1008
Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys			
325	330	335	
aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag			1056
Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys			
340	345	350	
tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca			1104
Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro			
355	360	365	
atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg			1152
Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu			
370	375	380	
ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa			1200
Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln			
385	390	395	400
tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt			1248
Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly			
405	410	415	
gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca			1296
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala			
420	425	430	
tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg			1344
Cys Gly Glu Leu Asp Asn Glu Ala Glu Val Arg Lys Ala Arg Arg			
435	440	445	
ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa			1392
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys			
450	455	460	

aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag			1440
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu			
465	470	475	480
tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct			1488
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala			
485	490	495	
tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra			1536
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa			
500	505	510	
gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn			1584
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa			
515	520	525	
cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat			1632
His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp			
530	535	540	
gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt			1680
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser			
545	550	555	560
gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca			1728
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala			
565	570	575	
atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg			1776
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp			
580	585	590	
gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt			1824
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe			
595	600	605	
tac cca ctt gat gtt tat ggt gtt aag aaa gca cca aaa cgg aaa			1872
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys			
610	615	620	
gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc			1920
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu			
625	630	635	640
atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa			1968
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu			
645	650	655	

ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa	660	665	670	2016
aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Leu Phe	675	680	685	2064
gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu	690	695	700	2112
ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu	705	710	715	2160
ata tta tac ggg atg agg att tca tat tca aag gcg aaa atg ctt Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu	725	730	735	2208
gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp	740	745	750	2256
agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys	755	760	765	2304
gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu	770	775	780	2352
cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu	785	790	795	2400
gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys	805	810	815	2448
tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His	820	825	830	2496
ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg	835	840	845	2544

att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc		2592	
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly			
850	855	860	
ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg		2640	
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val			
865	870	875	880
gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta		2688	
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Ser Glu Val Ala Leu			
885	890	895	
gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca		2736	
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro			
900	905	910	
aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag		2784	
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu			
915	920	925	
tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag		2832	
Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Pro Cys Gly Lys			
930	935	940	
ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac		2880	
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr			
945	950	955	960
atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg		2928	
Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val			
965	970	975	
cgt ttc cat cac aag agg tag		2949	
Arg Phe His His Lys Arg			
980			

<210> 2
<211> 982
<212> PRT
<213> Zea mays

<400> 2
Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu

20

25

30

Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
85 90 95

Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
100 105 110

Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
115 120 125

Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
130 135 140

Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
145 150 155 160

Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
165 170 175

Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
180 185 190

Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
195 200 205

Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gln
210 215 220

Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
225 230 235 240

Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
245 250 255

Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
260 265 270

Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala

275

280

285

Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
290 295 300

Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320

Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335

Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350

Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
355 360 365

Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380

Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400

Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
405 410 415

Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430

Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
435 440 445

Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
450 455 460

Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
465 470 475 480

Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
 485 490 495

Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
 500 505 510

Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
515 520 525

His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp

530 535 540
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
545 550 555 560
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
565 570 575
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
580 585 590
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
595 600 605
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
610 615 620
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
625 630 635 640
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
645 650 655
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
660 665 670
Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
675 680 685
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
690 695 700
Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
705 710 715 720
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
725 730 735
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
740 745 750
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
755 760 765
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
770 775 780
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu

785	790	795	800
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys			
805	810	815	
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His			
820	825	830	
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg			
835	840	845	
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly			
850	855	860	
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val			
865	870	875	880
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu			
885	890	895	
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro			
900	905	910	
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu			
915	920	925	
Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys			
930	935	940	
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr			
945	950	955	960
Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val			
965	970	975	
Arg Phe His His Lys Arg			
980			

```
<210> 3
<211> 474
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(474)
```

<400> 3
aac aag atg cta tta tgg cac ggt tca agg ttg acg aat ttt gtg gga 48
Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
1 5 10 15

att ctt agt caa ggg cta aga att gca cct cct gag gca cct gtt act 96
Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
20 25 30

ggc tat atg ttc ggc aaa ggc ctc tac ttt gca gat cta gta agc aag 144
Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
35 40 45

agc gca caa tac tgt tat gtg gat agg aat aat cct gta ggt ttg atg 192
Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
50 55 60

ctt ctt tct gag gtt gct tta gga gac atg tat gaa cta aag aaa gcc 240
Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
65 70 75 80

acg tcc atg gac aaa cct cca aga ggg aag cat tcg acc aag gga tta 288
Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
85 90 95

ggc aaa acc gtg cca ctg gag tca gag ttt gtg aag tgg agg gat gat 336
Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
100 105 110

gtc gta gtt ccc tgc ggc aag ccg gtg cca tca tca att agg agc tct 384
Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
115 120 125

gaa ctc atg tac aat gag tac atc gtc tac aac aca tcc cag gtg aag 432
Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
130 135 140

atg cag ttc ttg ctg aag gtg cgt ttc cat cac aag agg tag 474
Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
145 150 155

<210> 4
<211> 157
<212> PRT
<213> Zea mays

<400> 4

Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
1 5 10 15

Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
20 25 30

Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
35 40 45

Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
50 55 60

Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
65 70 75 80

Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
85 90 95

Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
100 105 110

Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
115 120 125

Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
130 135 140

Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
145 150 155

<210> 5
<211> 530
<212> DNA
<213> Zea mays

<400> 5
ctcgtgcaag tcatgccggc cccctatcgcaaggaccag ctccgtcttg gcaagatgg 60
tcaggcgtca cagttcgacg gttcatgcc gatgtggAAC catgccagggt gcatttcag 120
caagaagaac cagataaaat ccgttgacga tggtaaggg atagatgcac tttagatgg 180
tgcataagag aagatacgaa actacgttgg gagtgccctca gctggcacaa gttctacagc 240
tgctccctcct gagaaatgta caattgagat tgctccatct gcccgtactt catgttagacg 300
atgcagtgaa aagattacaa aaggatcggt ccgtcttca gctaagcttg agagtgaagg 360

tcccaagggt ataccatggt atcatgcaa ctgtttctt gaggtatccc cgtctgcaac 420
tggtgagaag ttctcaggct gggatacttt gtccgatgag gataagagaa ccatgctcga 480
tcttgtaaa aaagatgttgc aacaacaatga acaaaaataag ggttccaagc 530